

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/574,827
Source: IFWP
Date Processed by STIC: 5/4/06

ENTERED



IFWP

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/574,827

DATE: 05/04/2006
TIME: 13:36:02

Input Set : A:\14875-158US1sq.txt
Output Set: N:\CRF4\05042006\J574827.raw

3 <110> APPLICANT: Hayasaka, Akira
4 Igawa, Tomoyuki
5 Sekimori, Yasuo
8 <120> TITLE OF INVENTION: Method of stabilizing protein solutions
10 <130> FILE REFERENCE: 14875-158US1
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/574,827
C--> 12 <141> CURRENT FILING DATE: 2006-04-06
12 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/014919
13 <151> PRIOR FILING DATE: 2004-10-08
15 <150> PRIOR APPLICATION NUMBER: JP 2003-351410
16 <151> PRIOR FILING DATE: 2003-10-09
18 <160> NUMBER OF SEQ ID NOS: 18
20 <170> SOFTWARE: PatentIn version 3.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 1779
24 <212> TYPE: DNA
25 <213> ORGANISM: Homo sapiens
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (1)..(1779)
30 <223> OTHER INFORMATION:
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34 Met Glu Phe Gly Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly
35 1 5 10 15
37 gtc cag tgt gag gtc cag ctg ttg gat tct ggg gga ggc ttg gta cag 96
38 Val Gln Cys Glu Val Gln Leu Leu Asp Ser Gly Gly Gly Leu Val Gln
39 20 25 30
41 cct ggg ggg tgc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttt 144
42 Pro Gly Gly Cys Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
43 35 40 45
45 agc agc tgt gcc atg agc tgg gtc cgc cag gct cca ggg aag ggg ctg 192
46 Ser Ser Cys Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
47 50 55 60
49 gag tgg gtc tca gct att agt ggt agt ggt ggt agc aca tac tac gca 240
50 Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Ser Thr Tyr Tyr Ala
51 65 70 75 80
53 gac tcc gtg aag ggc cgg ttc acc atc tcc aga gac aaa tcc aag aac 288
54 Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Lys Ser Lys Asn
55 85 90 95
57 acg ttg tat ctg caa atg aac agc ctg aga gcc gag gac acg gcc gta 336
58 Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
59 100 105 110

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61	tat tac tgt gcg aaa ggt ggc aac gat att ttg act ggt tat tat gct	384
62	Tyr Tyr Cys Ala Lys Gly Gly Asn Asp Ile Leu Thr Gly Tyr Tyr Ala	
63	115 120 125	
65	tgg ggc cag gga acc ctc gtc acc gtc tcc tca ggg agt gca tcc gcc	432
66	Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Ser Ala Ser Ala	
67	130 135 140	
69	cca acc ctt ttc ccc ctc gtc tcc tgt gag aat tcc ccg tcg gat agg	480
70	Pro Thr Leu Phe Pro Leu Val Ser Cys Glu Asn Ser Pro Ser Asp Thr	
71	145 150 155 160	
73	agc agc gtg gcc gtt ggc tgc ctc gca cag gac ttc ctt ccc gac tcc	528
74	Ser Ser Val Ala Val Gly Cys Leu Ala Gln Asp Phe Leu Pro Asp Ser	
75	165 170 175	
77	atc act ttc tcc tgg aaa tac aag aac aac tct gac atc agc agc acc	576
78	Ile Thr Phe Ser Trp Lys Tyr Lys Asn Asn Ser Asp Ile Ser Ser Thr	
79	180 185 190	
81	cgg ggc ttc cca tca gtc ctg aga ggg ggc aag tac gca gcc acc tca	624
82	Arg Gly Phe Pro Ser Val Leu Arg Gly Lys Tyr Ala Ala Thr Ser	
83	195 200 205	
85	cag gtg ctg ctg cct tcc aag gac gtc atg cag ggc aca gac gaa cac	672
86	Gln Val Leu Leu Pro Ser Lys Asp Val Met Gln Gly Thr Asp Glu His	
87	210 215 220	
89	gtg gtg tgc aaa gtc cag cac ccc aac ggc aac aaa gaa aag aac gtg	720
90	Val Val Cys Lys Val Gln His Pro Asn Gly Asn Lys Glu Lys Asn Val	
91	225 230 235 240	
93	cct ctt cca gtg att gct gag ctg cct ccc aaa gtg agc gtc ttc gtc	768
94	Pro Leu Pro Val Ile Ala Glu Leu Pro Pro Lys Val Ser Val Phe Val	
95	245 250 255	
97	cca ccc cgc gac ggc ttc ttc ggc aac ccc cgc aag tcc aag ctc atc	816
98	Pro Pro Arg Asp Gly Phe Phe Gly Asn Pro Arg Lys Ser Lys Leu Ile	
99	260 265 270	
101	tgc cag gcc acg ggt ttc agt ccc cgg cag att cag gtg tcc tgg ctg	864
102	Cys Gln Ala Thr Gly Phe Ser Pro Arg Gln Ile Gln Val Ser Trp Leu	
103	275 280 285	
105	cgc gag ggg aag cag gtg ggg tct ggc gtc acc acg gac cag gtg cag	912
106	Arg Glu Gly Lys Gln Val Gly Ser Gly Val Thr Thr Asp Gln Val Gln	
107	290 295 300	
109	gct gag gcc aaa gag tct ggg ccc acg acc tac aag gtg acc agc aca	960
110	Ala Glu Ala Lys Glu Ser Gly Pro Thr Thr Tyr Lys Val Thr Ser Thr	
111	305 310 315 320	
113	ctg acc atc aaa gag agc gac tgg ctc ggc cag agc atg ttc acc tgc	1008
114	Leu Thr Ile Lys Glu Ser Asp Trp Leu Gly Gln Ser Met Phe Thr Cys	
115	325 330 335	
117	cgc gtg gat cac agg ggc ctg acc ttc cag cag aat gcg tcc tcc atg	1056
118	Arg Val Asp His Arg Gly Leu Thr Phe Gln Gln Asn Ala Ser Ser Met	
119	340 345 350	
121	tgt gtc ccc gat caa gac aca gcc atc cgg gtc ttc gcc atc ccc cca	1104
122	Cys Val Pro Asp Gln Asp Thr Ala Ile Arg Val Phe Ala Ile Pro Pro	
123	355 360 365	
125	tcc ttt gcc agc atc ttc ctc acc aag tcc acc aag ttg acc tgc ctg	1152

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126 Ser Phe Ala Ser Ile Phe Leu Thr Lys Ser Thr Lys Leu Thr Cys Leu			
127 370	375	380	
129 gtc aca gac ctg acc acc tat gac agc gtg acc atc tcc tgg acc cgc			1200
130 Val Thr Asp Leu Thr Thr Tyr Asp Ser Val Thr Ile Ser Trp Thr Arg			
131 385	390	395	400
133 cag aat ggc gaa gct gtg aaa acc cac acc aac atc tcc gag agc cac			1248
134 Gln Asn Gly Glu Ala Val Lys Thr His Thr Asn Ile Ser Glu Ser His			
135 405	410	415	
137 ccc aat gcc act ttc agc gcc gtg ggt gag gcc agc atc tgc gag gat			1296
138 Pro Asn Ala Thr Phe Ser Ala Val Gly Glu Ala Ser Ile Cys Glu Asp			
139 420	425	430	
141 gac tgg aat tcc ggg gag agg ttc acg tgc acc gtg acc cac aca gac			1344
142 Asp Trp Asn Ser Gly Glu Arg Phe Thr Cys Thr Val Thr His Thr Asp			
143 435	440	445	
145 ctg ccc tcg cca ctg aag cag acc atc tcc cgg ccc aag ggg gtg gcc			1392
146 Leu Pro Ser Pro Leu Lys Gln Thr Ile Ser Arg Pro Lys Gly Val Ala			
147 450	455	460	
149 ctg cac agg ccc gat gtc tac ttg ctg cca cca gcc cgg gag cag ctg			1440
150 Leu His Arg Pro Asp Val Tyr Leu Leu Pro Pro Ala Arg Glu Gln Leu			
151 465	470	475	480
153 aac ctg cgg gag tcg gcc acc atc acg tgc ctg gtg acg ggc ttc tct			1488
154 Asn Leu Arg Glu Ser Ala Thr Ile Thr Cys Leu Val Thr Gly Phe Ser			
155 485	490	495	
157 ccc gcg gac gtc ttc gtg cag tgg atg cag agg ggg cag ccc ttg tcc			1536
158 Pro Ala Asp Val Phe Val Gln Trp Met Gln Arg Gly Gln Pro Leu Ser			
159 500	505	510	
161 ccg gag aag tat gtg acc agc gcc cca atg cct gag ccc cag gcc cca			1584
162 Pro Glu Lys Tyr Val Thr Ser Ala Pro Met Pro Glu Pro Gln Ala Pro			
163 515	520	525	
165 ggc cgg tac ttc gcc cac agc atc ctg acc gtg tcc gaa gag gaa tgg			1632
166 Gly Arg Tyr Phe Ala His Ser Ile Leu Thr Val Ser Glu Glu Glu Trp			
167 530	535	540	
169 aac acg ggg gag acc tac acc tgc gtg gtg gcc cat gag gcc ctg ccc			1680
170 Asn Thr Gly Glu Thr Tyr Thr Cys Val Val Ala His Glu Ala Leu Pro			
171 545	550	555	560
173 aac agg gtc acc gag agg acc gtg gac aag tcc acc ggt aaa ccc acc			1728
174 Asn Arg Val Thr Glu Arg Thr Val Asp Lys Ser Thr Gly Lys Pro Thr			
175 565	570	575	
177 ctg tac aac gtg tcc ctg gtc atg tcc gac aca gct ggc acc tgc tac			1776
178 Leu Tyr Asn Val Ser Leu Val Met Ser Asp Thr Ala Gly Thr Cys Tyr			
179 580	585	590	
181 tga			1779
184 <210> SEQ ID NO: 2			
185 <211> LENGTH: 592			
186 <212> TYPE: PRT			
187 <213> ORGANISM: Homo sapiens			
189 <400> SEQUENCE: 2			
190 Met Glu Phe Gly Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly			
191 1	5	10	15

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192 Val Gln Cys Glu Val Gln Leu Leu Asp Ser Gly Gly Gly Leu Val Gln
 193 20 25 30
 194 Pro Gly Gly Cys Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
 195 35 40 45
 196 Ser Ser Cys Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 197 50 55 60
 198 Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Ser Thr Tyr Tyr Ala
 199 65 70 75 80
 200 Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Lys Ser Lys Asn
 201 85 90 95
 202 Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
 203 100 105 110
 204 Tyr Tyr Cys Ala Lys Gly Gly Asn Asp Ile Leu Thr Gly Tyr Tyr Ala
 205 115 120 125
 206 Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Ser Ala Ser Ala
 207 130 135 140
 208 Pro Thr Leu Phe Pro Leu Val Ser Cys Glu Asn Ser Pro Ser Asp Thr
 209 145 150 155 160
 210 Ser Ser Val Ala Val Cys Leu Ala Gln Asp Phe Leu Pro Asp Ser
 211 165 170 175
 212 Ile Thr Phe Ser Trp Lys Tyr Lys Asn Asn Ser Asp Ile Ser Ser Thr
 213 180 185 190
 214 Arg Gly Phe Pro Ser Val Leu Arg Gly Gly Lys Tyr Ala Ala Thr Ser
 215 195 200 205
 216 Gln Val Leu Leu Pro Ser Lys Asp Val Met Gln Gly Thr Asp Glu His
 217 210 215 220
 218 Val Val Cys Lys Val Gln His Pro Asn Gly Asn Lys Glu Lys Asn Val
 219 225 230 235 240
 220 Pro Leu Pro Val Ile Ala Glu Leu Pro Pro Lys Val Ser Val Phe Val
 221 245 250 255
 222 Pro Pro Arg Asp Gly Phe Phe Gly Asn Pro Arg Lys Ser Lys Leu Ile
 223 260 265 270
 224 Cys Gln Ala Thr Gly Phe Ser Pro Arg Gln Ile Gln Val Ser Trp Leu
 225 275 280 285
 226 Arg Glu Gly Lys Gln Val Gly Ser Gly Val Thr Thr Asp Gln Val Gln
 227 290 295 300
 228 Ala Glu Ala Lys Glu Ser Gly Pro Thr Thr Tyr Lys Val Thr Ser Thr
 229 305 310 315 320
 230 Leu Thr Ile Lys Glu Ser Asp Trp Leu Gly Gln Ser Met Phe Thr Cys
 231 325 330 335
 232 Arg Val Asp His Arg Gly Leu Thr Phe Gln Gln Asn Ala Ser Ser Met
 233 340 345 350
 234 Cys Val Pro Asp Gln Asp Thr Ala Ile Arg Val Phe Ala Ile Pro Pro
 235 355 360 365
 236 Ser Phe Ala Ser Ile Phe Leu Thr Lys Ser Thr Lys Leu Thr Cys Leu
 237 370 375 380
 238 Val Thr Asp Leu Thr Thr Tyr Asp Ser Val Thr Ile Ser Trp Thr Arg
 239 385 390 395 400
 240 Gln Asn Gly Glu Ala Val Lys Thr His Thr Asn Ile Ser Glu Ser His

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241	405	410	415	
242	Pro Asn Ala Thr Phe Ser Ala Val Gly Glu Ala Ser Ile Cys Glu Asp			
243	420	425	430	
244	Asp Trp Asn Ser Gly Glu Arg Phe Thr Cys Thr Val Thr His Thr Asp			
245	435	440	445	
246	Leu Pro Ser Pro Leu Lys Gln Thr Ile Ser Arg Pro Lys Gly Val Ala			
247	450	455	460	
248	Leu His Arg Pro Asp Val Tyr Leu Leu Pro Pro Ala Arg Glu Gln Leu			
249	465	470	475	480
250	Asn Leu Arg Glu Ser Ala Thr Ile Thr Cys Leu Val Thr Gly Phe Ser			
251	485	490	495	
252	Pro Ala Asp Val Phe Val Gln Trp Met Gln Arg Gly Gln Pro Leu Ser			
253	500	505	510	
254	Pro Glu Lys Tyr Val Thr Ser Ala Pro Met Pro Glu Pro Gln Ala Pro			
255	515	520	525	
256	Gly Arg Tyr Phe Ala His Ser Ile Leu Thr Val Ser Glu Glu Glu Trp			
257	530	535	540	
258	Asn Thr Gly Glu Thr Tyr Thr Cys Val Val Ala His Glu Ala Leu Pro			
259	545	550	555	560
260	Asn Arg Val Thr Glu Arg Thr Val Asp Lys Ser Thr Gly Lys Pro Thr			
261	565	570	575	
262	Leu Tyr Asn Val Ser Leu Val Met Ser Asp Thr Ala Gly Thr Cys Tyr			
263	580	585	590	
266	<210> SEQ ID NO: 3			
267	<211> LENGTH: 723			
268	<212> TYPE: DNA			
269	<213> ORGANISM: Homo sapiens			
271	<220> FEATURE:			
272	<221> NAME/KEY: CDS			
273	<222> LOCATION: (1)..(723)			
274	<223> OTHER INFORMATION:			
W-->	276 <400> 3			
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278	Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser			
279	1 5 10 15			
281	ggt gcc tac ggg gac atc gtg atg acc cag tct cca gac tcc ctg gct			96
282	Gly Ala Tyr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala			
283	20 25 30			
285	gtg tct ctg ggc gag agg gcc acc atc aac tgc aag tcc agc cag agt			144
286	Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser			
287	35 40 45			
289	gtt tta tac agc tcc aac aat aag aac tac tta gct tgg tac cag cag			192
290	Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln			
291	50 55 60			
293	aaa cca gga cag cct aag ctg ctc att tac tgg gca tct acc cgg			240
294	Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg			
295	65 70 75 80			
297	gaa tcc ggg gtc cct gac cga ttc agt ggc agc ggg tct ggg aca gat			288
298	Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp			

RAW SEQUENCE LISTING ERROR SUMMARY
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:7,8,9,10,11,12,13,14,15,16,17,18

VERIFICATION SUMMARY

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Input Set : A:\14875-158US1sq.txt

Output Set: N:\CRF4\05042006\J574827.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:32 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:30
L:276 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:274
L:388 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:386